

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/424,705

DATE: 03/26/2001

TIME: 09:02:29

Input Set : A:\Pto.amc

Output Set: N:\CRF3\03232001\I424705.raw

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4 <110> APPLICANT: LITTLE, MELVYN
5      KIPRIYANOV, SERGEY
6      MOLDENHAUER, GERHARD
7      DEUTSCHES KREBSFORSCHUNGSZEUTRUM
9 <120> TITLE OF INVENTION: MUTATED OKT3 ANTIBODY
12 <130> FILE REFERENCE: 035280047US00
14 <140> CURRENT APPLICATION NUMBER: 09/424,705
15 <141> CURRENT FILING DATE: 2000-06-02
17 <150> PRIOR APPLICATION NUMBER: PCT/DE98/01409
18 <151> PRIOR FILING DATE: 1998-05-22
20 <160> NUMBER OF SEQ ID NOS: 7
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 909
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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30 <221> NAME/KEY: CDS
31 <222> LOCATION: (28)...(900)
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34 gaattcatta aagaggagaa attaacc atg aaa tac cta ttg cct acg gca gcc      54
35             Met Lys Tyr Leu Leu Pro Thr Ala Ala
36             1           5
38 gct ggc ttg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag      102
39 Ala Gly Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
40 10          15          20          25
42 ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag      150
43 Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
44          30          35          40
46 atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac      198
47 Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
48          45          50          55
50 tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att      246
51 Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
52          60          65          70
54 aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag      294
55 Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys
56          75          80          85
58 gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg caa ctg      342
59 Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu
60 90          95          100          105
62 agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca aga tat      390
63 Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr
64          110          115          120
66 tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc act ctc      438
67 Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu
68          125          130          135

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70	aca	gtc	tcc	tca	gcc	aaa	aca	aca	ccc	aag	ctt	gaa	gaa	ggt	gaa	ttt	486
71	Thr	Val	Ser	Ser	Ala	Lys	Thr	Thr	Pro	Lys	Leu	Glu	Glu	Gly	Glu	Phe	
72											140	145	150				
74	tca	gaa	gca	cgc	gta	gat	atc	gtg	ctc	act	cag	tct	cca	gca	atc	atg	534
75	Ser	Glu	Ala	Arg	Val	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	
76											155	160	165				
78	tct	gca	tct	cca	ggg	gag	aag	gtc	acc	atg	acc	tgc	agt	gcc	agc	tca	582
79	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Ser	Ala	Ser	Ser	
80	170						175				180			185			
82	agt	gtt	agt	tac	atg	aac	tgg	tac	cag	cag	aag	tca	ggc	acc	tcc	ccc	630
83	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Thr	Ser	Pro	
84						190				195			200				
86	aaa	aga	tgg	att	tat	gac	aca	tcc	aaa	ctg	gct	tct	gga	gtc	cct	gct	678
87	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Leu	Ala	Ser	Gly	Val	Pro	Ala	
88						205				210			215				
90	cac	ttc	agg	ggc	agt	ggg	tct	ggg	acc	tct	tac	tct	ctc	aca	atc	agc	726
91	His	Phe	Arg	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	
92						220			225			230					
94	ggc	atg	gag	gct	gaa	gat	gct	gcc	act	tat	tac	tgc	cag	cag	tgg	agt	774
95	Gly	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	
96						235			240			245					
98	agt	aac	cca	tcc	acg	tcc	ggc	tgc	tcg	ggg	aca	aag	ttg	gaa	ata	aac	822
99	Ser	Asn	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	Asn	Arg	
100	250					255			260			265					
102	gct	gat	act	gca	cca	act	gga	tcc	gaa	caa	aag	ctg	atc	tca	gaa	gaa	870
103	Ala	Asp	Thr	Ala	Pro	Thr	Gly	Ser	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	
104						270			275			280					
106	gac	cta	aac	tca	cat	cac	cat	cac	cat	cac	taatctaga						909
107	Asp	Leu	Asn	Ser	His												
108						285			290								
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112	<211> LENGTH: 291																
113	<212> TYPE: PRT																
114	<213> ORGANISM: Homo sapiens																
116	<400> SEQUENCE: 2																
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118	1				5				10			15					
119	Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	
120					20				25			30					
121	Leu	Ala	Arg	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	
122					35				40			45					
123	Tyr	Thr	Phe	Thr	Arg	Tyr	Thr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	
124					50				55			60					
125	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	
126	65				70				75			80					
127	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Thr	Asp	Lys	
128					85				90			95					
129	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	
130					100				105			110					

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131 Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu
 132 115 120 125
 133 Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
 134 130 135 140
 135 Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Asp Ile
 136 145 150 155 160
 137 Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
 138 165 170 175
 139 Val Thr Met Thr Cys Ser Ala Ser Ser Val Ser Tyr Met Asn Trp
 140 180 185 190
 141 Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
 142 195 200 205
 143 Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
 144 210 215 220
 145 Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
 146 225 230 235 240
 147 Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
 148 245 250 255
 149 Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly
 150 260 265 270
 151 Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His
 152 275 280 285
 153 His His His
 154 290
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 157 <211> LENGTH: 906
 158 <212> TYPE: DNA
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 161 <220> FEATURE:
 162 <221> NAME/KEY: CDS
 163 <222> LOCATION: (28)...(897)
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 167 Met Lys Tyr Leu Leu Pro Thr Ala Ala
 168 1 5
 170 gct ggc ttg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag 102
 171 Ala Gly Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
 172 10 15 20 25
 174 ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag 150
 175 Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
 176 30 35 40
 178 atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac 198
 179 Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
 180 45 50 55
 182 tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att 246
 183 Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
 184 60 65 70
 186 aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag 294
 187 Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys

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188	75	80	85	
190	gac aag gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg			342
191	Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met			
192	90	95	100	105
194	caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca			390
195	Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala			
196	110	115	120	
198	aga tat tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc			438
199	Arg Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr			
200	125	130	135	
202	act ctc aca gtc tcc tca gcc aaa aca aca ccc aag ctt ggc ggt gat			486
203	Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp			
204	140	145	150	
206	atc ttg ctc acc caa act cca gct tct ttg gct gtg tct cta ggg cag			534
207	Ile Leu Leu Thr Gln Thr Pro Ala Ser Leu Ala Val Ser Leu Gly Gln			
208	155	160	165	
210	agg gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat ggt			582
211	Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly			
212	170	175	180	185
214	gat agt tat ttg aac tgg tac caa cag att cca gga cag cca ccc aaa			630
215	Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys			
216	190	195	200	
218	ctc ctc atc tat gat gca tcc aat cta gtt tct ggg atc cca ccc agg			678
219	Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg			
220	205	210	215	
222	ttt agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat cct			726
223	Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro			
224	220	225	230	
226	gtg gag aag gtg gat gct gca acc tat cac tgt cag caa agt act gag			774
227	Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu			
228	235	240	245	
230	gat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa cgg gct			822
231	Asp Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala			
232	250	255	260	265
234	gat gct gcg gcc gct gga tcc gaa caa aag ctg atc tca gaa gaa gac			870
235	Asp Ala Ala Ala Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp			
236	270	275	280	
238	cta aac tca cat cac cat cac cat taaagatct			906
239	Leu Asn Ser His His His His His			
240	285	290		
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244	<211> LENGTH: 290			
245	<212> TYPE: PRT			
246	<213> ORGANISM: Homo sapiens			
248	<400> SEQUENCE: 4			
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250	1	5	10	15
251	Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Ala Glu			
252	20	25	30	

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253 Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
 254 35 40 45
 255 Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
 256 50 55 60
 257 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
 258 65 70 75 80
 259 Asn Tyr Asn Gln Lys Phe Lys Asp Lys Asp Lys Ala Thr Leu Thr Thr
 260 85 90 95
 261 Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
 262 100 105 110
 263 Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
 264 115 120 125
 265 Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala
 266 130 135 140
 267 Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Leu Leu Thr Gln Thr Pro
 268 145 150 155 160
 269 Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
 270 165 170 175
 271 Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
 272 180 185 190
 273 Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
 274 195 200 205
 275 Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
 276 210 215 220
 277 Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
 278 225 230 235 240
 279 Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
 280 245 250 255
 281 Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Ala Gly Ser
 282 260 265 270
 283 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His His
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 285 His His
 286 290
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 300 1 5
 302 gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag 102
 303 Ala Gly Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
 304 10 15 20 25
 306 ctg cag cag tct ggg gct gag ctg gtg agg cct ggg tcc tca gtg aag 150

VERIFICATION SUMMARY DATE: 03/26/2001
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